

**STIC Biotechnology Systems Branch**

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/553,459  
Source: IFWP  
Date Processed by STIC: 1/19/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

| ERROR DETECTED  | SUGGESTED CORRECTION   | SERIAL NUMBER: <u>10/553,459</u> |
|---|--|----------------------------------|
| <b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b> |  |                                  |
| 1 <u>  </u> Wrapped Nucleics<br><u>  </u> Wrapped Aminos  | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."   |                                  |
| 2 <u>  </u> Invalid Line Length   | The rules require that a line not exceed 72 characters in length. This includes white spaces.  |                                  |
| 3 <u>  </u> Misaligned Amino<br><u>  </u> Numbering   | The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.  |                                  |
| 4 <u>  </u> Non-ASCII   | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.   |                                  |
| 5 <u>  </u> Variable Length   | Sequence(s) <u>      </u> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.   |                                  |
| 6 <u>  </u> PatentIn 2.0<br><u>  </u> "bug"   | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <u>      </u> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.   |                                  |
| 7 <u>  </u> Skipped Sequences<br>(OLD RULES)  | Sequence(s) <u>      </u> missing. If intentional, please insert the following lines for each skipped sequence:<br>(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)<br>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>This sequence is intentionally skipped<br>Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |                                  |
| 8 <u>  </u> Skipped Sequences<br>(NEW RULES)  | Sequence(s) <u>      </u> missing. If intentional, please insert the following lines for each skipped sequence.<br><210> sequence id number<br><400> sequence id number<br>000   |                                  |
| 9 <u>  </u> Use of n's or Xaa's<br>(NEW RULES)  | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.   |                                  |
| 10 <u>  </u> Invalid <213><br>Response  | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)   |                                  |
| 11 <u>  </u> Use of <220>   | Sequence(s) <u>      </u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules   |                                  |
| 12 <u>  </u> PatentIn 2.0<br>"bug"  | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.  |                                  |
| 13 <u>  </u> Misuse of n/Xaa  | "n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>  |                                  |



IFWP

do not include  
these headings. Do not include page numbers.

see pp 1-4

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/553,459

DATE: 01/23/2007  
TIME: 16:44:18

Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF4\01232007\J553459.raw

see item 4 on  
Error summary  
sheet

W--> 1 WO 2004/092396  
W--> 2 PCT/US2004/011622

delete at beginning of the  
file

Does Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: Hallenbeck, Paul  
5 Hampton, Garret  
6 Hay, Carl  
7 Huang, Ying  
8 Jakubczak, John  
9 Phipps, Sandrina

see item 2  
on Error summary sheet

W--> 10 <120> TITLE OF INVENTION: FLAP ENDONUCLEASE 1 (FEN1) REGULATORY SEQUENCES AND USES  
THEREOF

12 <130> FILE REFERENCE: GTIN-021WO  
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/553,459  
C--> 14 <141> CURRENT FILING DATE: 2005-10-17  
14 <150> PRIOR APPLICATION NUMBER: 60/463,148  
15 <151> PRIOR FILING DATE: 2003-04-15  
W--> 16 <160> NUMBER OF SEQ ID: 8  
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Suggestion: Consult  
Sequence  
Rules for  
valid format

#### ERRORED SEQUENCES

19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 2259  
21 <212> TYPE: DNA  
22 <213> ORGANISM: H. sapiens  
W--> 23 <400> SEQUENCE: 1  
24 catgcggtta tcaaggagcc tgggtgctgcc gtgaaacaga ggctgatttt agccccgaaa 60  
25 tgtagctgca gatcaatggc ccttatttagc attttctgag gccataatc tgaccactat 120  
26 gaaaacgtga ctaaaggtag gaactctctg cctgagaaaa accacataca agaaaaagtt 180  
27 tgcctacaat ttccggagct ttgtggacca gtgtctatag acaccaagct gagaaccccc 240  
28 gctataagtc actgactggt ggtacccaga tctcaatata tttttttttt gacggagtct 300  
29 catttttttg acggcgctct actctgtcgc ccgggctgga gggcagtgga acgatctcgg 360  
30 ctcaactgaa cctctgcctc ccgggttcta gagattctca tacctcagcc tctcgagtag 420  
31 ctggggactat aggattacag gtgcgcacca ccacatctaa tttttgtatt tttagtagag 480  
32 attggggtttt gccatgctgg ccaggatggt cttgaattcc tgacctcagg tgatctgcct 540  
33 gctcgggctt cccaaagtac tgagattaca ggtgtgagtt gccgcgcccc ggctcaattt 600  
34 tttttttttt ccagacagtc ttgctctatc gccaggctg gagtgcctgg agtgcagtg 660  
35 tgccaactcg gctcaactga agctccgcct tctgggttca agtgattatc ctgcctcagc 720  
36 ctcccagagca gctgggatta cagggtgtgaa ccaccatgcc cggctaattt tttgtatttt 780  
E--> 37 taggagagac aggggtttcac cttgctggcc aggtctgtg tgaactctg acctcctgat 840  
38 ccgctgcct cagcctccca aagtgcctgg attacaggag tgaaccaccg cgctggccc 900  
39 tcaatttcta attcagtag ttccctacta cctatgctat tatggaatct tgtgagctat 960  
E--> 40 ggtcaagaca ttcaagttct ggttctgagt aatctgagc tgagtaaagc gactgtaata 1020  
41 tctatttcac agaactgaaa aataagaaag atgatgaatc aaagcatcta gtgcctagca 1080

Invalid  
nucleic acid  
designators

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/553,459

DATE: 01/23/2007  
TIME: 16:44:18

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\01232007\J553459.raw

```

E--> 42 gggagtattt tgctcaacag gtatttgctt ccttcctaag gctgtaggga agatgargag 1140
E--> 43 ataatgtctt ttatgaaaga gggctgtaaa cgtaaagatc tgtacaaatg ttaacttcat 1200
44 tgtcaccggg cagccaatgc ttctaaaatc cagaacataa caactctaga gaagtaaact 1260
45 gccccattg ttctgagaca ctggaattca attcagtaaa caatcacggc ccccttcccc 1320
46 caaaatgata aagacaatca ctgccattta ttgagcttcc aattacgggc cctctgtttg 1380
47 gcaactgagaa tacaaagatg aatagacatc atcccagagc tagatgcgcg tcagacgggtg 1440
48 gtcactagga ggcgtggccg aaaacaaaga agtccatgga acgtggccag agatctgtac 1500
49 agaggctgtg ggcgtcctta ggaaagtctg gccaaagtgc tgagagttgg aagtgttca 1560
50 ccaataaaca tttgccagg gcattgtagg atgggcacgg gtccggcaga agaactttcc 1620
51 aaataaagat aacacaccac cgataacaga qatatacaaa ctggaaggta ttcaaaattc 1680
E--> 52 gcccacgccc tctcgccctt agaaatcgcg agctgagaaa cctaaggagt tcatggcaag 1740
53 gggcttcccc cttccccacc cttcagccca agccggaggt tccaggagcg tctagccctc 1800
54 tggatctccg gcgtctgagg agataagcgc ggtgtgggtc agaccccgag gggctctcgc 1860
E--> 55 atctccgtct ggaactcccc tcaacgctct caccattttg ccccgcgagg gctaatccgc 1920
56 cgctccgcca ccggaagaac acgtcgacag gagcaggcgc ctagcacaac cggaaaagga 1980
57 agtgcctccg gcgcaagtgg cattgagggg cttgtagtcc tgcgatttcg ggtgtagagg 2040
58 gagcaggggc ctgcgggggac ctgggtgtggg tggagtgggg acaagcgggtg gagaagggtg 2100
E--> 59 1
E--> 62 WO 2004/092396
E--> 65 Pct/us2004/01162
E--> 66 2
E--> 69 cgcaggggtc gctgagagac tctgttctcc ctggagggac tgggtgccat gagagcagcc 2160
E--> 70 gtctgagggg acgcagcctg cactacgcgc cccaagaggc tgtgcgtggc gagcaggtca 2220
E--> 71 cgtgacggga gcgcgggctt tggaaggcgg ctgaacgctc
E--> 72 2259

```

invalid

invalid

delete

2259

see item 1 on Error Summary Sheet

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/553,459

DATE: 01/23/2007  
TIME: 16:44:19

FYI

Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF4\01232007\J553459.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 71

10/553,459 4

<210> 8  
<211> 270

2

WO 2004/092396

*delete*

PCT/US2004/011  
622

<212> DNA

5

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/553,459

DATE: 01/23/2007  
TIME: 16:44:19

Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF4\01232007\J553459.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:  
L:2 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:  
L:10 M:283 W: Missing Blank Line separator, <120> field identifier  
L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:16 M:283 W: Missing Blank Line separator, <160> field identifier  
L:23 M:283 W: Missing Blank Line separator, <400> field identifier  
L:37 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:40 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:43 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:52 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:55 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:59 M:254 E: No. of Bases conflict, this line has no nucleotides.  
M:254 Repeated in SeqNo=1  
L:62 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6  
L:62 M:112 C: (48) String data converted to lower case,  
L:65 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7  
M:112 Repeated in SeqNo=1  
L:72 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2259 Found:2269 SEQ:1  
L:78 M:283 W: Missing Blank Line separator, <400> field identifier  
L:87 M:283 W: Missing Blank Line separator, <400> field identifier  
L:97 M:283 W: Missing Blank Line separator, <400> field identifier  
L:103 M:283 W: Missing Blank Line separator, <400> field identifier  
L:109 M:283 W: Missing Blank Line separator, <400> field identifier  
L:115 M:283 W: Missing Blank Line separator, <400> field identifier  
L:119 M:259 W: Allowed number of lines exceeded, <211> LENGTH:  
L:122 M:259 W: Allowed number of lines exceeded, <211> LENGTH:  
L:125 M:259 W: Allowed number of lines exceeded, <211> LENGTH:  
L:126 M:259 W: Allowed number of lines exceeded, <211> LENGTH:  
L:131 M:283 W: Missing Blank Line separator, <400> field identifier